AMENDMENTS TO THE CLAIMS:

Please amend the claims as follows:

1. **(Currently amended) A promoter comprising an [[An]]** isolated DNA molecule ~~**comprising a nucleotide sequence**~~ **having a nucleotide sequence of at least 300 nucleotides, wherein the** ~~**selected from the group consisting of:**~~

[[(a) a]] nucleotide sequence **[[that]]** has at least **[[90%]] 95%** sequence identity to the sequence set forth in SEQ ID NO:8**[[; and]] or the**

[[(b) a]] nucleotide sequence **[[that]]** hybridizes to the sequence set forth in SEQ ID NO:8 under ~~**at least**~~ high stringency conditions.

Claims 2-69. (Cancelled).

70. **(Currently amended) A promoter comprising an [[An]]** isolated DNA molecule ~~**comprising a nucleotide sequence**~~ **having a nucleotide sequence of at least 300 nucleotides, wherein the nucleotide sequence [[that]]** has at least **[[90%]] 95%** sequence identity to the sequence set forth in SEQ ID NO:8 or **the nucleotide sequence** hybridizes to the sequence set forth in SEQ ID NO:8 under ~~**at least**~~ high stringency conditions, wherein the nucleotide sequence is further selected from the group consisting of:

a) a nucleotide sequence set forth in SEQ ID NO:6;

b) a nucleotide sequence that has at least **[[90%]] 95%** sequence identity to the sequence set forth in SEQ ID NO:6;

c) a nucleotide sequence that hybridizes to the sequence set forth in SEQ ID NO:6 under ~~**at least**~~ high stringency conditions;

d) the nucleotide sequence set forth in SEQ ID NO:7;

e) a nucleotide sequence that has at least **[[90%]] 95%** sequence identity to the sequence set forth in SEQ ID NO:7; and

f) a nucleotide sequence that hybridizes to the sequence set forth in SEQ ID NO:7 under ~~**at least**~~ high stringency conditions.

71. **(Currently amended)** The ~~**DNA molecule**~~ **promoter** of claim 1, wherein the

nucleotide sequence **as set forth in SEQ ID NO:6 or 7** is ~~**obtained**~~ **derived** from a virus.

72. **(Currently amended)** The ~~**DNA molecule**~~ **promoter** of claim 1, wherein the nucleotide sequence **as set forth in SEQ ID NO:6 or 7** is ~~**obtained**~~ **derived** from a badnavirus.

73. **(Currently amended)** **A monocotyledonous plant comprising a nucleotide sequence according to** ~~**The DNA molecule of**~~ claim 71, wherein **a nucleic acid operably linked to** the nucleotide sequence **as set forth in SEQ ID NO:6 or 7** is expressed constitutively in **[[a]] the** monocotyledonous plant.

74. **(Currently amended)** **A non-graminaceous monocotyledonous plant comprising a nucleotide sequence according to** ~~**The DNA molecule of**~~ claim 71, wherein **a nucleic acid operably linked to** the nucleotide sequence **as set forth in SEQ ID NO:6 or 7** is expressed constitutively in **[[a]] the** non-graminaceous monocotyledonous plant.

75. **(Currently amended)** The **non-graminaceous monocotyledonous plant** ~~**DNA molecule**~~ of claim 74, wherein the non-graminaceous monocotyledonous plant is selected from the group consisting of *Musaceae*, taro, ginger, onions, garlic, pineapple, bromeliaeds, palms, orchids, lilies and irises.

76. **(Currently amended)** The **non-graminaceous monocotyledonous plant** ~~**DNA molecule**~~ of claim 74, wherein the non-graminaceous monocotyledonous plant is taro.

77. **(Currently amended)** The ~~**DNA molecule**~~ **promoter** of claim 1, wherein **[[the]]** the nucleotide sequence is as set forth in SEQ ID NO:6 or 7.

78-80. (Cancelled).

81. (Withdrawn) An isolated polynucleotide comprising a nucleotide sequence that corresponds or is complementary to at least a portion of the sequence set forth in SEQ ID NO:1 or to a variant thereof wherein the portion is at least 90 nucleotides in length and wherein the variant displays at least 80% sequence identity to the at least a portion.

82. (Withdrawn) polynucleotide of claim 81, wherein the variant displays at least 85% sequence identity to at the least a portion.

83. (Withdrawn) The polynucleotide of claim 82, wherein the variant displays at least 80% sequence identity to a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of SEQ ID NO:3, 4 and 5.

84. (Withdrawn) The polynucleotide of claim 81, wherein the variant hybridises to at least a portion of the sequence set forth in SEQ ID NO:1, which is at least 18 nucleotides in length, under at least high stringency conditions.

85. (Withdrawn) The polynucleotide of claim 84, wherein the variant hybridises to a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of SEQ ID NO:3, 4 and 5 under at least high stringency conditions.

86. (Withdrawn) An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

(i) at least a portion of the sequence set forth in SEQ ID NO:4, wherein the portion is at least six amino acids in length;

(ii) at least a portion of a variant that displays at least 55% sequence identity to the sequence set forth in SEQ ID NO:4, wherein the portion is at least 15 amino acid residues in length;

(iii) at least a portion of the sequence set forth in SEQ ID NO:5, wherein the portion is at least seven amino acids in length;

(iv) at least a portion of a variant that displays at least 65% sequence identity to the sequence set forth in SEQ ID NO:5, wherein the portion is at least 30 amino acid residues in length;

(v) least a portion of the sequence set forth in SEQ ID NO:6, wherein the portion is at least 16 amino acid residues in length;

(vi) at least a portion of a variant that displays at least 70% sequence identity to the sequence set forth in SEQ ID NO:6, wherein the portion is at least 30 amino acid residues in length.

87. **(Currently amended)** A chimeric DNA construct comprising the nucleotide sequence of claim 1, **as set forth in SEQ ID NO:6 or 7,** operably linked to a ~~**foreign or endogenous**~~ DNA sequence to be transcribed.

88. **(Currently amended)** The construct of claim 87, further comprising a 3' non-translated sequence that is operably linked to the ~~**foreign or endogenous**~~ DNA sequence **to be transcribed** and that functions in plant cells to terminate transcription and/or to cause addition of a polyadenylated nucleotide sequence to the 3' end of a transcribed RNA sequence.

89. **(Currently amended)** A chimeric DNA construct comprising the nucleotide sequence of claim 70, wherein the nucleotide sequence **as set forth in SEQ ID NO:6 or 7** is operably linked to a ~~**foreign or endogenous**~~ DNA sequence to be transcribed.

90. (Cancelled).

91. **(Currently amended)** The construct of claim 87, wherein the nucleotide sequence **hybridizes to the sequence [[is]]** as set forth in SEQ ID NO:6 or 7 **under high stringency conditions**.

92. (Cancelled).

93. **(Currently amended)** The construct of claim 87, wherein the ~~**foreign or endogenous**~~ DNA sequence **to be transcribed** encodes a structural or regulatory protein.

94. **(Currently amended)** The construct of claim 87, wherein the ~~**foreign or endogenous**~~ DNA sequence **to be transcribed** encodes a transcript capable of modulating expression of a corresponding target gene.

95. **(Currently amended)** The construct of claim 94, wherein the transcript comprises a transcribed region ~~**aimed at**~~ **for** downregulating the expression of the corresponding target gene.

96. **(Currently amended)** The construct of claim 94, wherein the transcript comprises a transcribed region **comprising** ~~**that represents a**~~ molecule**s** selected from the group

consisting of a sense suppression molecule, an antisense RNA, a ribozyme and an RNAi molecule.

97. (Previously presented) The construct of claim 87, further comprising an enhancer element.

98. (Previously presented) The construct of claim 87, further comprising a leader sequence which modulates mRNA stability.

99. **(Currently amended)** The construct of claim 87, further comprising **a nucleic acid sequence encoding** a targeting sequence for targeting a protein product of the ~~**foreign or endogenous**~~ DNA sequence **to be transcribed** to an intracellular compartment within plant cells or to an extracellular environment.

100. (Previously presented) The construct of claim 87, further comprising a selectable marker gene.

101. (Previously presented) The construct of claim 87, further comprising a screenable marker gene.

102. **(Currently amended)** **A host cell transformed with a** **[[The]]** construct of claim 87, wherein **a nucleic acid operably linked to** the promoter or biologically active fragment or variant is constitutively expressed in a host cell.

103. **(Currently amended)** The **host cell** ~~**construct**~~ of claim 102, wherein the host cell is a plant cell.

104. **(Currently amended)** The **host cell** ~~**construct**~~ of claim 102, wherein the host cell is a monocotyledonous plant cell.

105. **(Currently amended)** The **host cell** ~~**construct**~~ of claim 102, wherein the host cell is a non-graminaceous monocotyledonous plant cell.

106. **(Currently amended)** The **host cell** ~~**construct**~~ of claim 102, wherein the host cell is a non-graminaceous monocotyledonous plant cell selected from the group consisting of *Musaceae*, taro, ginger, onions, garlic, pineapple, bromeliaeds, palms, orchids, lilies and irises.

107. **(Currently amended)** The **host cell** ~~**construct**~~ of claim 102~~, wherein the host cell~~ is a graminaceous monocotyledonous plant cell.

108. **(Currently amended)** The **host cell** ~~**construct**~~ of claim 102~~, wherein the host cell~~ is a dicotyledonous plant cell.

109. (Withdrawn) A method for gene expression in a plant, comprising introducing into a plant cell a chimeric DNA construct comprising an isolated promoter or biologically active fragment thereof or variant of these, wherein the promoter is naturally located upstream of a transcribable DNA sequence which hybridises to a nucleic acid probe derived from the polynucleotide sequence set forth in SEQ ID NO:1 under at least high stringency conditions, wherein the promoter or biologically active fragment or variant is operably linked to a foreign or endogenous DNA sequence to be transcribed.

110. (Withdrawn) A method for producing transformed plant cells, comprising:

(a) introducing into regenerable plant cells a chimeric DNA construct comprising an isolated promoter or biologically active fragment thereof or variant of these, wherein the promoter is naturally located upstream of a transcribable DNA sequence which hybridises to a nucleic acid probe derived from the polynucleotide sequence set forth in SEQ ID NO:1 under at least high stringency conditions, wherein the promoter or biologically active fragment or variant is operably linked to a foreign or endogenous DNA sequence to be transcribed, so as to yield transformed plant cells; and

(b) identifying or selecting transformed plant cells.

111. (Withdrawn) A method for selecting stable genetic transformants from transformed plant cells comprising:

(a) introducing into regenerable plant cells a chimeric DNA construct comprising an isolated promoter or biologically active fragment thereof or variant of these, wherein the promoter is naturally located upstream of a transcribable DNA sequence which hybridises to a nucleic acid probe derived from the polynucleotide sequence set forth in SEQ ID NO:1 under at least high stringency conditions, wherein the promoter or

biologically active fragment or variant is operably linked to a foreign or endogenous DNA sequence to be transcribed, so as to yield transformed plant cells; and

(b) identifying or selecting a transformed plant cell line from said transformed plant cells.

112. (Withdrawn) A method for producing a differentiated transgenic plant, comprising:

(a) introducing into regenerable plant cells a chimeric DNA construct comprising an isolated promoter or biologically active fragment thereof or variant of these, wherein the promoter is naturally located upstream of a transcribable DNA sequence which hybridises to a nucleic acid probe derived from the polynucleotide sequence set forth in SEQ ID NO:1 under at least high stringency conditions, wherein the promoter or biologically active fragment or variant is operably linked to a foreign or endogenous DNA sequence to be transcribed, so as to yield regenerable transformed plant cells;

(b) identifying or selecting a population of transformed plant cells; and

(c) regenerating a differentiated transgenic plant from the population.

113. (Withdrawn) The method of claims 109, wherein the cells are dicotyledonous plant cells.

114. (Withdrawn) The method claim 109, wherein the cells are monocotyledonous plant cells.

115. (Withdrawn) The method of claim 109, wherein the cells are graminaceous monocotyledonous plant cells.

116. (Withdrawn) The method of claim 109, wherein the cells are non-graminaceous monocotyledonous plant cells.

117. (Withdrawn) The method of claim 109, wherein expression of the chimeric DNA construct in the transformed cells imparts a phenotypic characteristic to the transformed cells.

118. (Withdrawn) The method of claim 109, wherein the construct comprises a selectable marker gene.

119. (Withdrawn) The method of claim 109, wherein the construct comprises a screenable marker gene.

120. (Withdrawn) The method of claim 112, wherein expression of the chimeric DNA construct renders the differentiated transgenic plant identifiable over the corresponding non-transgenic plant.

121. (Withdrawn) The method of claim 112, further comprising obtaining progeny from the differentiated transgenic plant.

122. (Withdrawn) Progeny obtained by the method of claim 121.

123. (Withdrawn) A plant part of the differentiated transgenic plant obtained from the method of claim 112, wherein the plant part contains the chimeric construct.

124. (Withdrawn) A differentiated transgenic plant regenerated from transformed plant cells obtained by the method of claim 110.

125. (Withdrawn) A transformed plant cell containing a chimeric DNA construct comprising an isolated plant promoter or biologically active fragment thereof or variant of these, wherein said promoter is naturally located upstream of a transcribable DNA sequence which hybridises to a nucleic acid probe derived from the polynucleotide sequence set forth in SEQ ID NO:1 under at least high stringency conditions, wherein said promoter or biologically active fragment or variant is operably linked to a foreign or endogenous DNA sequence to be transcribed.

126. (Withdrawn) A differentiated transgenic plant comprising plant cells containing a chimeric DNA construct comprising an isolated plant promoter or biologically active fragment thereof or variant of these, wherein said promoter is naturally located upstream of a transcribable DNA sequence which hybridises to a nucleic acid probe derived from the polynucleotide sequence set forth in SEQ ID NO:1 under at least high stringency conditions, wherein said promoter or biologically active fragment or variant is operably linked to a foreign or endogenous DNA sequence to be transcribed.

127. (Withdrawn) The transgenic plant of claim 126, wherein the plant is a dicotyledonous plant.

128. (Withdrawn) The transgenic plant of claim 126, wherein the plant is a monocotyledonous plant.

129. (Withdrawn) The transgenic plant of claim 126, wherein the plant is a graminaceous monocotyledonous plant.

130. (Withdrawn) The transgenic plant of claim 126, wherein the plant is a non-graminaceous monocotyledonous plant.

131. (Withdrawn) The transgenic plant of claim 126, wherein the construct comprises a selectable marker gene.

132. (Withdrawn) The transgenic plant of claim 126, wherein the construct comprises a screenable marker gene.

133. (Withdrawn) The transgenic plant of claim 126, wherein the expression of the chimeric DNA construct renders the differentiated transgenic plant identifiable over the corresponding non-transgenic plant.

134. (Withdrawn) A method of using of a chimeric DNA construct comprising an isolated plant promoter or biologically active fragment thereof or variant of these, wherein said promoter is naturally located upstream of a transcribable DNA sequence which hybridizes to a nucleic acid probe derived from the polynucleotide sequence set forth in SEQ ID NO:1 under at least high stringency conditions, wherein said promoter or biologically active fragment or variant is operably linked to a foreign or endogenous DNA sequence to be transcribed, in the production of a transformed plant cell, plant or plant part.

135. (Withdrawn) A method for diagnosing a badnaviral infection of a plant, comprising detecting the presence in a cell or tissue of the plant of (a) a nucleotide sequence that corresponds or is complementary to at least a portion of the nucleotide sequence set forth in SEQ ID NO:1 or 2, or of a variant of the nucleotide sequence, or (b) an amino acid sequence that corresponds to at least a portion of the sequence set forth in SEQ ID NO:3, 4 or 5, or of a variant of the amino acid sequence.

136. (Withdrawn) A method of screening for an agent that modulates badnaviral infection, the method comprising:

– contacting a preparation comprising:

(i) a polypeptide comprising an amino acid sequence that corresponds to at least a portion of the sequence set forth in SEQ ID NO: 3, 4 or 5, or of a variant of the sequence; or

(ii) a polynucleotide comprising a nucleotide sequence that corresponds or is complementary to at least a portion of the sequence set forth in SEQ ID NO:1 or 2, which polynucleotide is operably linked to a promoter; or

(iii) a polynucleotide comprising a reporter gene that is operably connected to a promoter comprising the sequence set forth in SEQ ID NO:6, 7, 8 or 9, with a test agent; and

– detecting a change in the level and/or functional activity of the polypeptide, or an expression product of the nucleotide sequence or of the reporter gene, relative to a normal or reference level and/or functional activity in the absence of the test agent.

137. (Withdrawn) The method of claim 136, wherein the agent inhibits or reduces badnavirus infection and the method comprises detecting a reduction in the level and/or functional activity of the polypeptide, or an expression product of the nucleotide sequence or of the reporter gene, relative to the normal or reference level and/or functional activity.

138. (Withdrawn) A method for treating and/or preventing badnaviral infection of a plant, comprising administering to the plant an agent that:

– reduces the level and/or functional activity of:

a polypeptide that comprises an amino acid sequence corresponding to at least a portion of the sequence set forth in SEQ ID NO: 3, 4 or 5, or of a variant of the sequence; or

an expression product of a nucleotide sequence that corresponds or is complementary to at least a portion of the sequence set forth in SEQ ID NO:1 or 2; or

– reduces the functional activity of a promoter that comprises the sequence set forth in any one of SEQ ID NO:6, 7, 8 or 9.